



POLITÉCNICA

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Department of
Electronic Engineering

Image processing methods for human brain connectivity analysis from in-vivo diffusion MRI

Ph.D. Thesis

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November 25th, 2015



As humans, we can identify galaxies light years away and we can study particles smaller than an atom, but we still haven't unlocked the mystery of the 3 lbs. of matter that sits between our ears.

Barack Obama, President of the United States, April 2013

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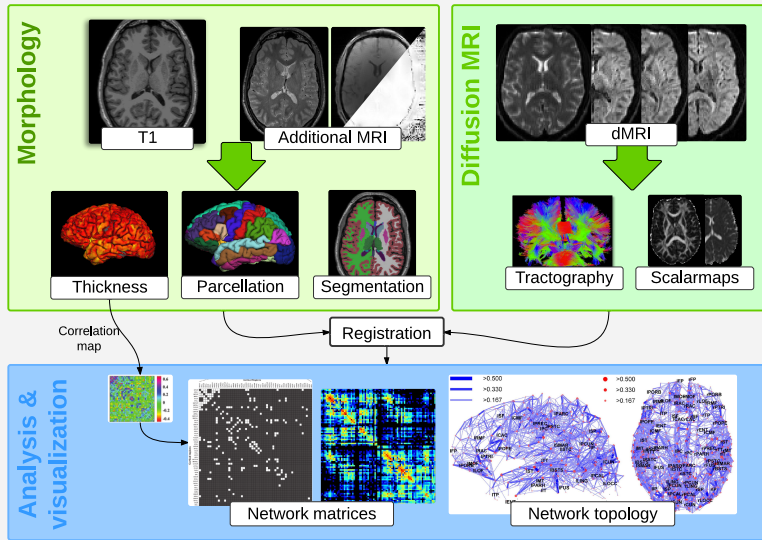
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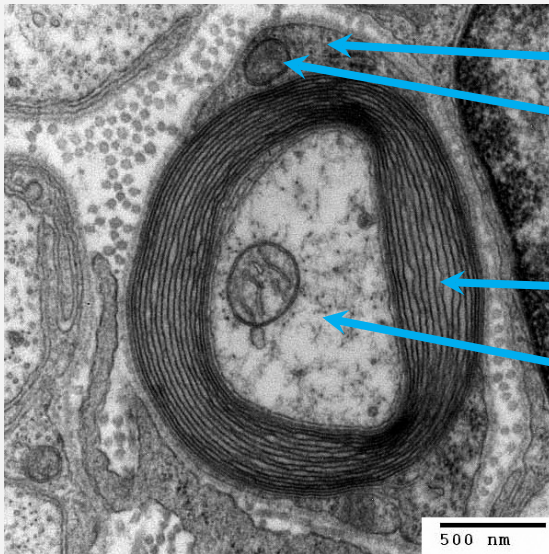
Context: the human connectome mapping

- ▶ The human brain is the organ system least known.
- ▶ In 2005 starts the quest of mapping the **human connectome**, the individual fingerprint of the “wiring” connecting regions of the brain.
- ▶ Expected to unveil **new biomarkers** for research (Sporns, 2012) and clinical application (Griffa et al., 2013).
- ▶ Enabling technology to map it **in-vivo**: diffusion MRI (dMRI, Le Bihan and Breton, 1985).
- ▶ Large funding initiatives: Human Brain Project (EU), BRAIN (US), etc.

Overview of the connectome extraction processing flow



Why/How it works?: microstructure of tissues



Schwann Cell

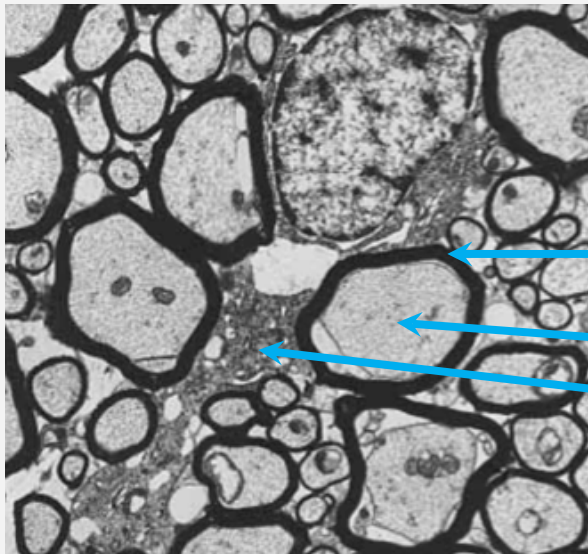
Nucleus of
Schwann Cell

Myelin Sheath

Axon

500 nm

Why/How it works?: microstructure of tissues



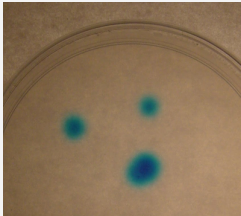
Myelin Sheath

Axon

Interstitium

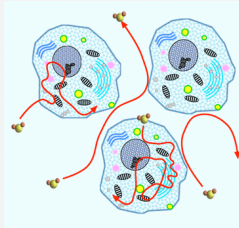
Why/How it works?: microstructure of tissues

CSF (cerebrospinal fluid)



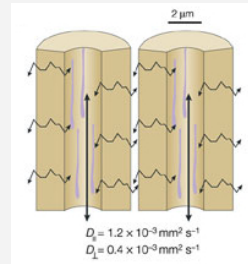
Free diffusion (only extracellular)

GM (grey matter)



Hindered diffusion (intra-, extra- and exchange)

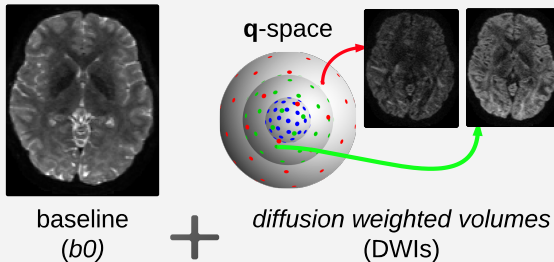
WM (white matter)



Restricted diffusion (confined in the axial orientation)

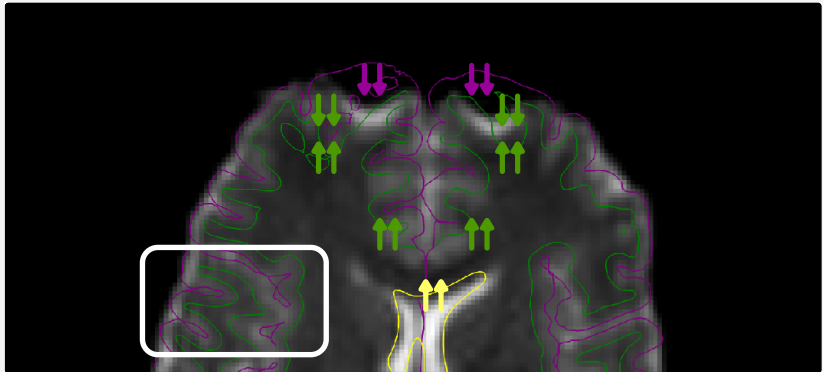
- Components of diffusion in the white-matter (WM): intracellular diffusion, extracellular diffusion and exchange between intra- and extra-cellular space.

Scanning the diffusion weighted volumes (DWIs)



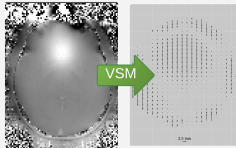
- The faster diffusion is in the sampled orientation (in the q -space) and voxel, the lesser signal registered in that voxel and DWI volume.
- Then, a model of diffusion orientation is fitted.
- The simplest model is **DTI** (Basser and Pierpaoli, 1996). It needs at least 6 DWIs. Generally: 32, or even more DWIs.

The origin of the problem: EPI distortion

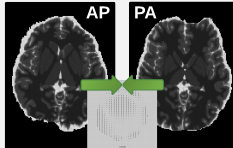


- dMRI is acquired with Echo-Planar Imaging (EPI).
- EPI is very fast, but introduces nonlinear distortion aligned with the phase-encoding (PE) direction.
- Magnitude of warping \propto inhomogeneity of field (B_0).

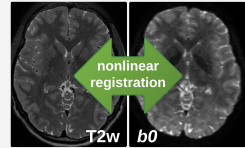
Option A: Susceptibility Distortion Correction (SDC) methods



FMB (Jezzard and Balaban, 1995)



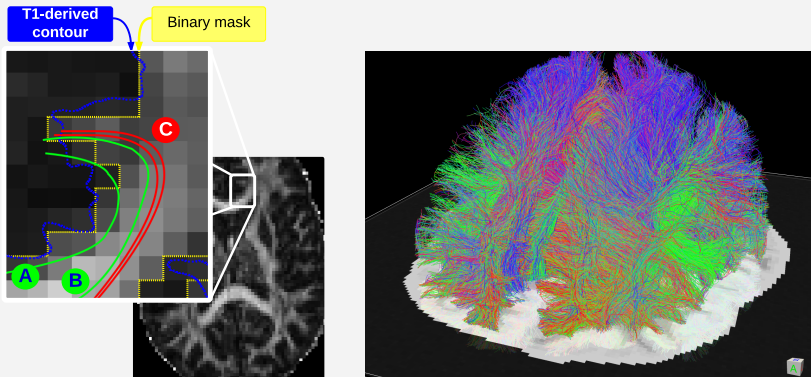
rPEB (Chiou and Nalciglu, 2000)



T2B (Kybic et al., 2000)

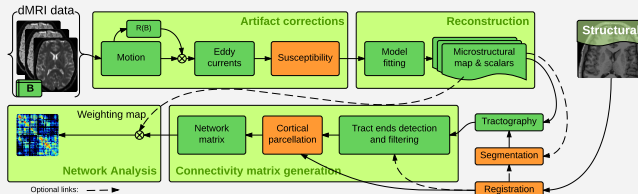
- ▶ All look for the underlying deformation field. The field is **nonzero only in the component of PE**.
- ▶ All need for **additional acquisitions**.
- ▶ Alternatives (Robson, Gore, and Constable, 1997), and many improvements (Irfanoglu et al., 2015).
- ▶ Retrospective correction requires resampling of DWIs with **unknown consequences**.

Option B: Image segmentation in native (dMRI) -space



- Early: WM-mask (FA thresholding) for termination criterium.
- Numerous segmentation methods have been proposed, without suitable results (noise, low resolution of dMRI, etc.).

Motivation



- Established connectome extraction pipelines are complex, and **unreliable** (Buchanan et al., 2014).
- Existing **validations are limited**:
 - **missing gold standards** and ground-truth datasets,
 - only test modules, with very **specific** benchmarks (e.g. accuracy),
 - many are **qualitative** (visual),
 - concerns with **data quality** (Lauzon et al., 2013).
- Model fitting (Jeurissen et al., 2014) and tractography (Smith et al., 2012) are **increasingly using structural information** (perform segmentation and registration earlier).

Objectives

General: **the characterization of the *susceptibility distortions*, the evaluation of existing correction methods and proposing alternatives** in the context of the connectome extraction.

Specific:

- ▶ A **comprehensive verification and validation framework** for connectivity pipelines.
- ▶ A **characterization of the susceptibility-derived distortions and their impact on whole-brain networks**.
- ▶ A **simultaneous registration and segmentation method** for dMRI data.

Hypothesis: distortions and SDCs have an important impact on connectivity analyses, oftentimes underestimated.

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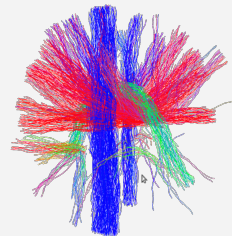
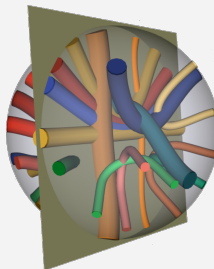
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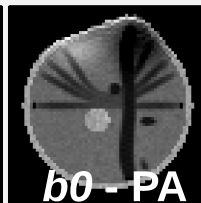
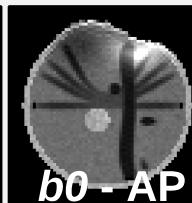
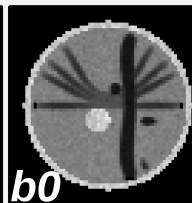
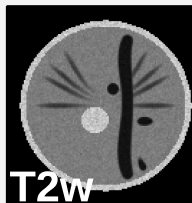
Publications

Gold standards: Phantomas

- ▶ 27 fiber bundles
- ▶ $70 \times 70 \times 70$ (voxels)
- ▶ $1.0 \times 1.0 \times 1.0$ (mm).
- ▶ Default: 64 DWIs ($b=3000\text{s/mm}^2$).
- ▶ Customizable \mathbf{q} -space sampling.
- ▶ 3695 voxels of pure WM
- ▶ 1192 voxels > 1 fiber bundles.
- ▶ HARDI Challenge, ISBI 2013.
- ▶ Caruyer et al., 2014.

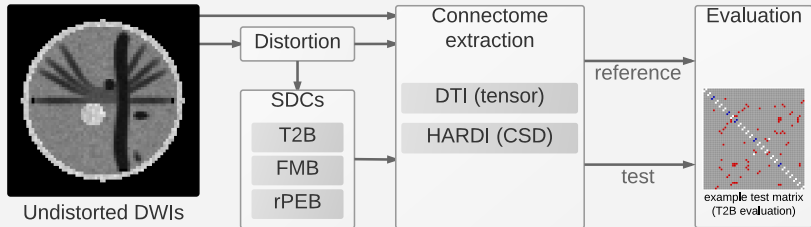


- ▶ Testing susceptibility distortions:



Experiment 1: methods

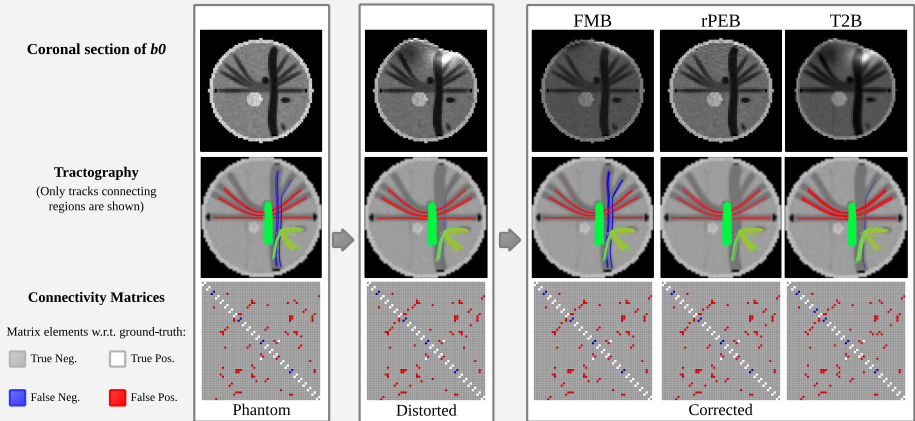
- ▶ 2 versions of *Phantom*s: 32 DWIs for DTI & 64 DWIs for HARDI.
- ▶ Comparing 3 SDCs: FMB, rPEB, and T2B.
- ▶ Distortion range $\max |\Delta y| = (3.80\text{--}7.60)$ mm.



- ▶ Early conclusion: DTI unsuitable for reconstructing *Phantom*s.

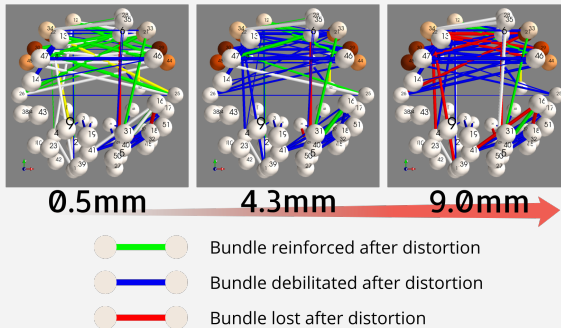
Experiment 1: results

- All SDCs under test improved detection.



Experiment 2: methods & results

- Only tested impact of distortion
- Wider distortion range, $\max |\Delta y| = (0.5\text{--}9.0)$ mm.
- **Networks change importantly** even with very small distortions.
- 27 connections (+ 40 false positives) is **not enough**.



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- Gold standards

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- Publications

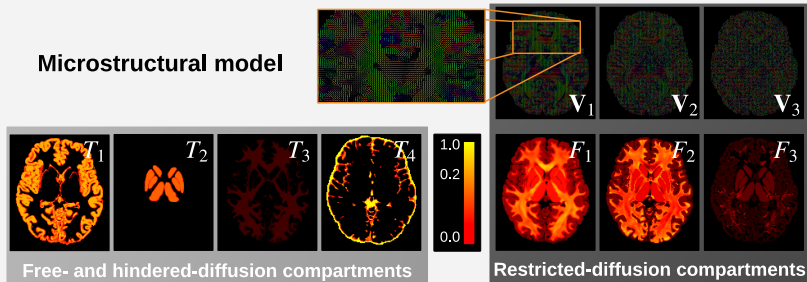
Data: The Human Connectome Project (HCP)

- ▶ Two large consortia under a 5yr. project of the NIH.
- ▶ Acquiring **high-standard**, research-oriented data (Van Essen and Ugurbil, 2012).
- ▶ Data are curated and preprocessed (Glasser et al., 2013). Therefore **distortion free**.
- ▶ We use them extensively to generate gold standards.

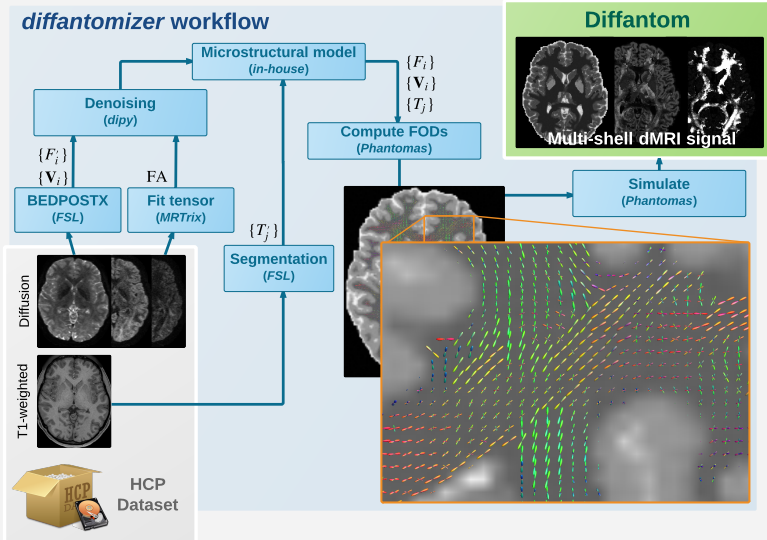


Diffantom: introduction & microstructural model

- ▶ Whole-brain phantoms are derived from real datasets.
- ▶ Inspired by Wilkins et al., 2015:
 - ▶ CHARMED (Assaf and Basser, 2005) model.
 - ▶ Real datasets are corrected for distortions.
- ▶ *Phantomas* simulates signal.
- ▶ Microstructural model derived from the real dataset:

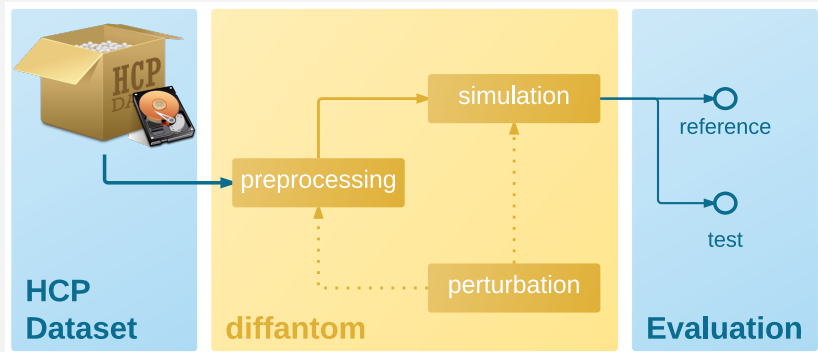


The diffantomizer workflow



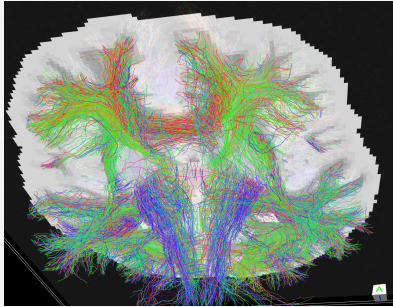
Use of Diffantom

- *Diffantom* is openly available (doi:10.5061/dryad.4p080).
- The *diffantomizer* workflow is open source.
- We created a *Diffantom* with emulated EPI distortion, following this model:

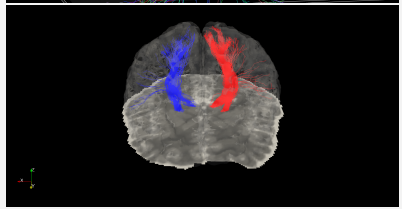
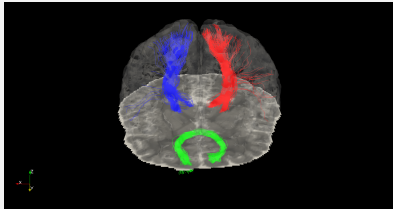
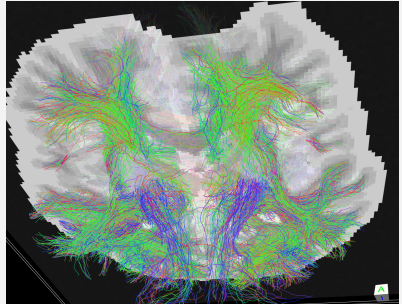


Diffantom: tractography and illustrative bundles

Undistorted



EPI distortion simulated



► Tractography using ACT, tracts segmentation using *track_querier* (Wassermann et al., 2013).

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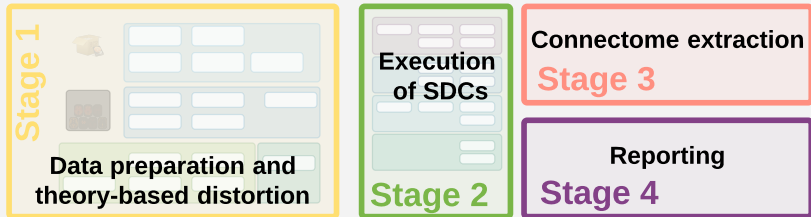
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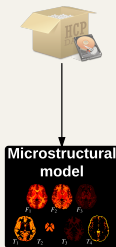
The PySDCev evaluation framework

- ▶ Aim: evaluating EPI distortions, and comparing SDCs at the whole-brain scale.
- ▶ Measures include investigating the impact on networks.
- ▶ Integrates the *diffantomizer*.

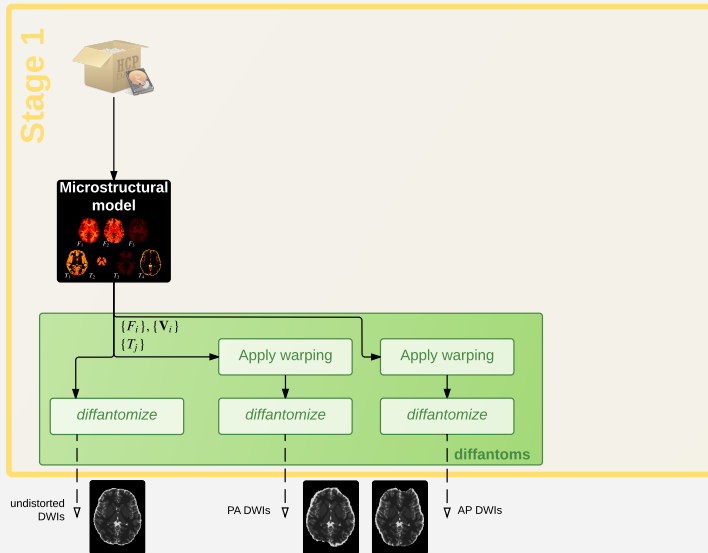


PySDCev, Stage 1

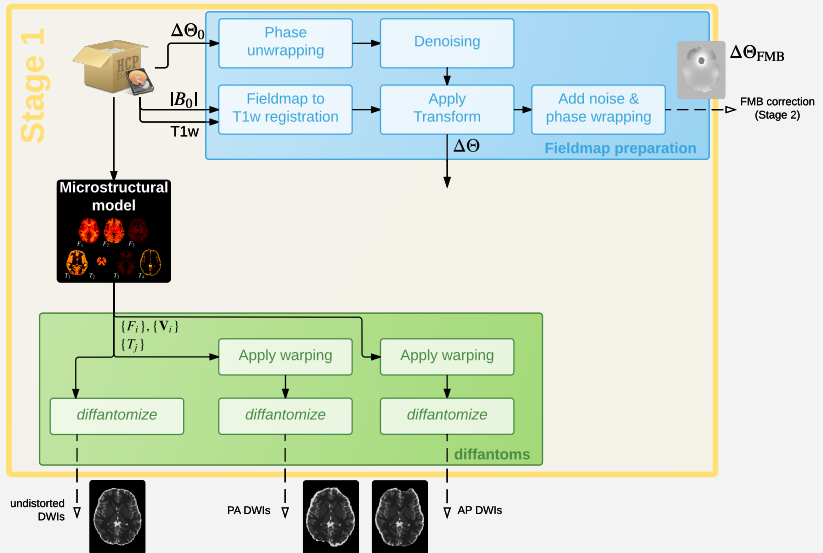
Stage 1



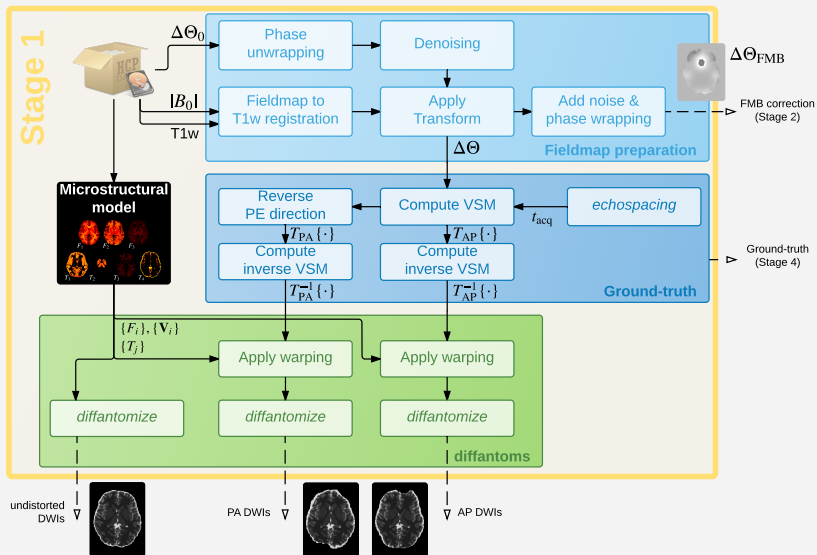
PySDCev, Stage 1



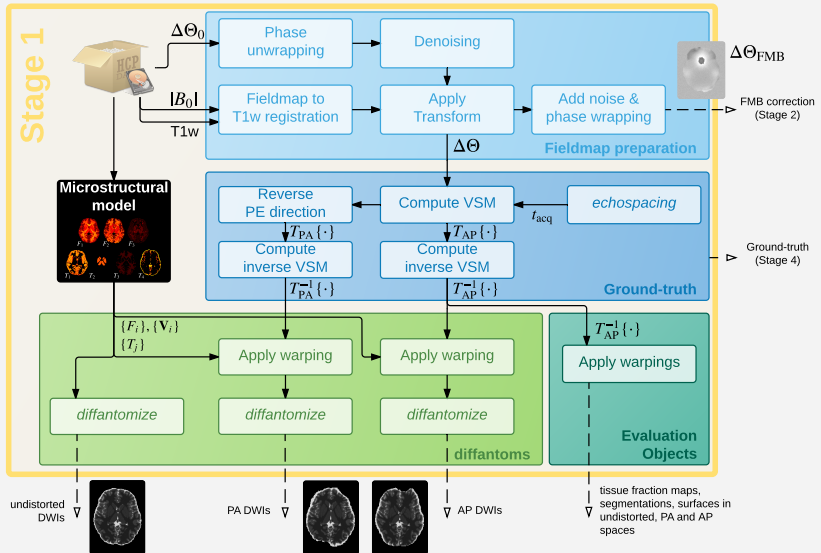
PySDCev, Stage 1



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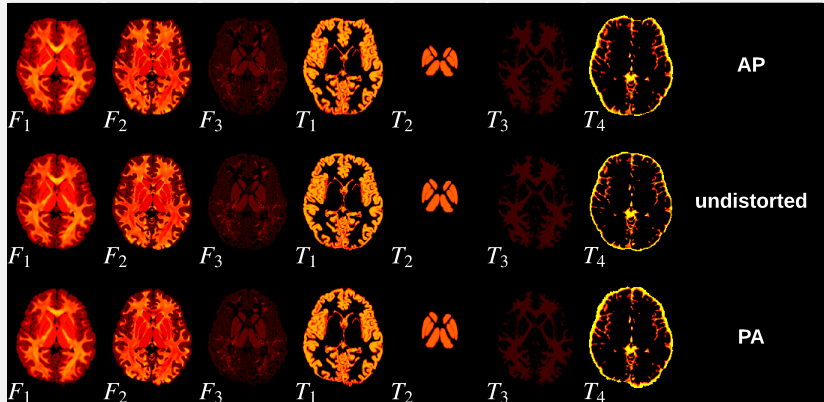


PySDCev, Stage 1



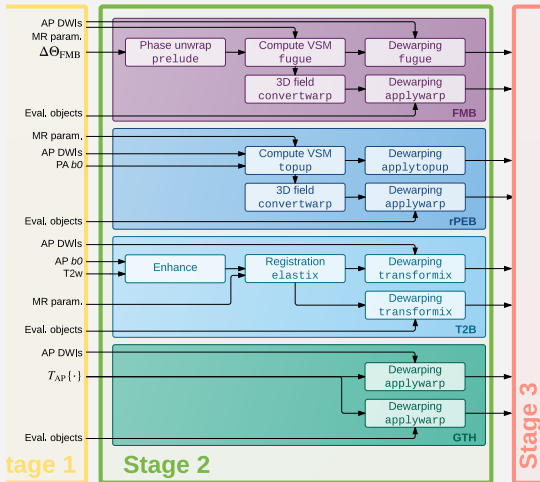
PySDCev, Stage 1

- How the microstructural model of *Diffantom* is distorted:



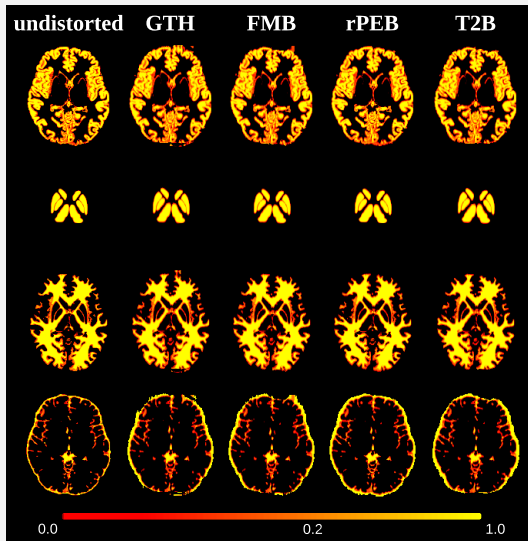
- ... ultimately avoiding DWI signal interpolation.

PySDCev, Stage 2



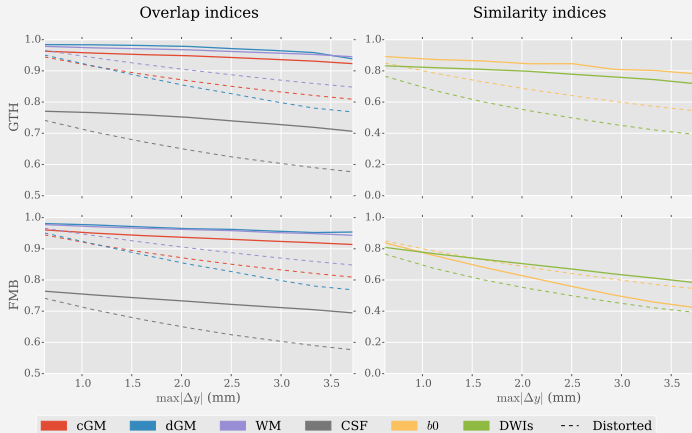
- GTH is a ground-truth reference workflow using the known distortion.

Results - Geometrical accuracy (visually)



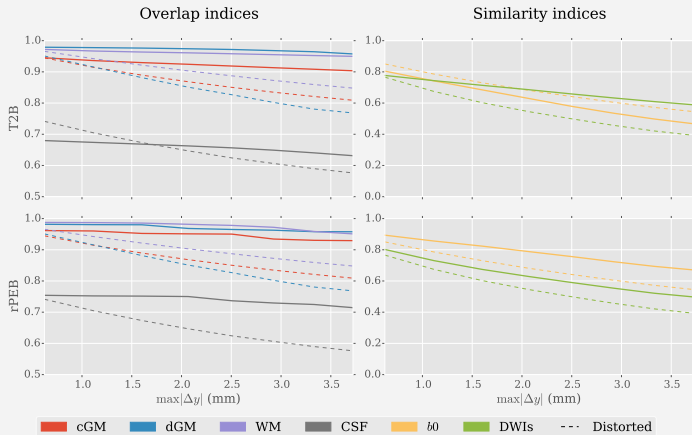
Results - Geometrical accuracy (quantitative)

- Quantitative evaluation of overlap of tissues, and similarity between original and recovered signal.

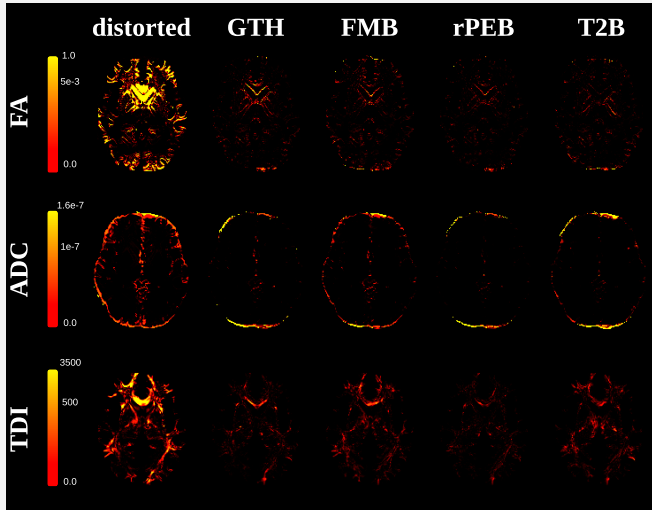


Results - Geometrical accuracy (quantitative)

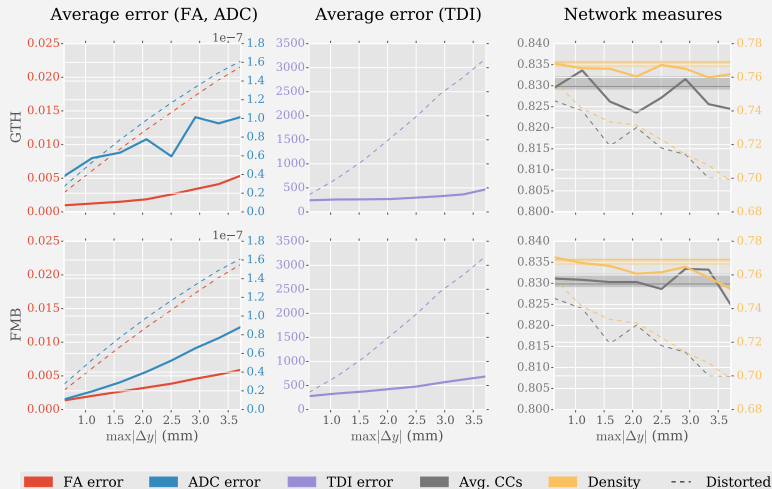
- Quantitative evaluation of overlap of tissues, and similarity between original and recovered signal.



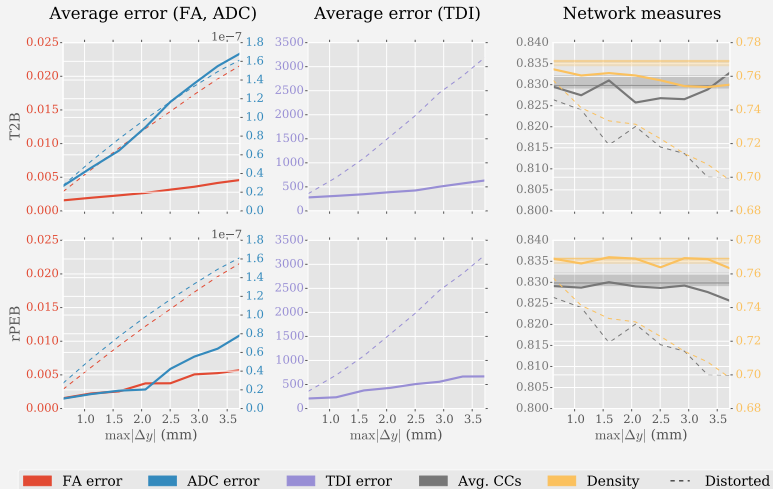
Results - Error maps (visually)



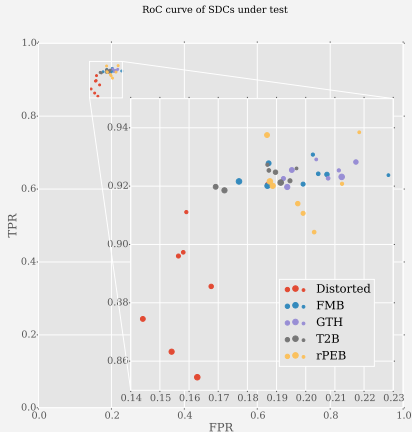
Results - Quantitative evaluation of impact (I)



Results - Quantitative evaluation of impact (II)



Results - RoC analysis



- Corrections **are not cost-less**: improvement on sensitivity implies a loss on specificity.
- The GTH distortion (using the known mapping) does not perform better than SDCs. Thus, **any interpolation of DWIs** introduces many FPs.

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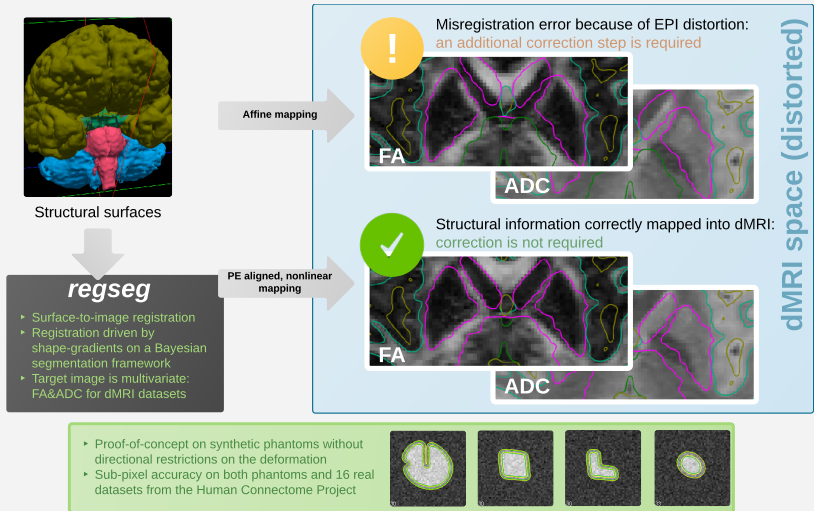
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Registration and segmentation model

- Registration to map a set of surfaces Γ into M :

$$U: \Gamma \subset \mathbb{R}^n \rightarrow M \subset \mathbb{R}^n$$

$$\mathbf{r} \mapsto \mathbf{r}' = \mathbf{r} + \mathbf{u}(\mathbf{r}).$$

- Bayes' rule on the regions Ω defined by the projected Γ :

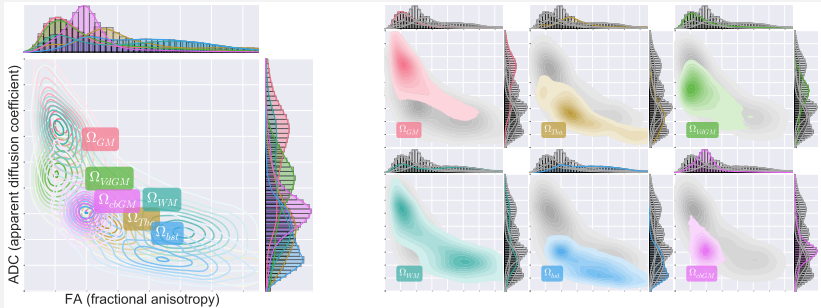
$$P(U | M, \Omega) = \frac{P(M | U, \Omega) P(U)}{P(M)}.$$

- Homogeneous regions Ω_l modeled with multivariate normal distributions:

$$P(M | U) = \prod_l \prod_{\mathbf{r} \in \Omega_l} \frac{1}{\sqrt{(2\pi)^C |\Sigma_l|}} e^{(-\frac{1}{2} \mathcal{D}_l^2(\mathbf{r}'))}.$$

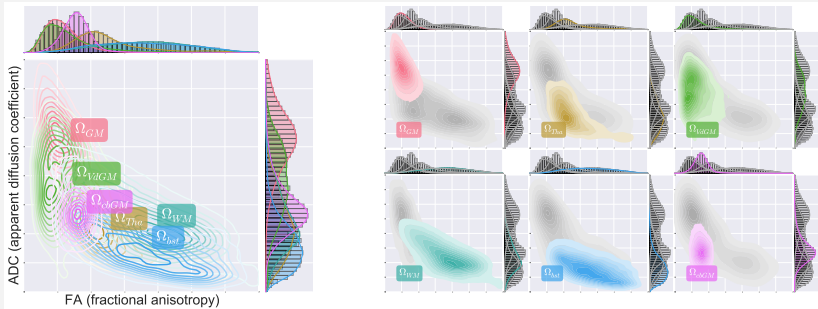
Visual inspection of the segmentation model

- Segmentation of six homogeneous regions Ω_l .
- Indirect minimization of covariances.
- Model with **undistorted** surfaces, imposed on **distorted** data:



Visual inspection of the segmentation model

- Segmentation of six homogeneous regions Ω_l .
- Indirect minimization of covariances.
- Model with **distorted** surfaces, fitted into **distorted** data:



Cost-function of regseg

- Mumford and Shah functional (1989), with the regularization term of Nagel and Enkelmann, 1986:

$$E(\mathbf{u}) = \text{Const.} + \underbrace{\sum_l \int_{\Omega_l} \mathcal{D}_l^2(\mathbf{f}') d\mathbf{r}}_{\text{Data term } (E_{\text{data}})} + \underbrace{\int_{\Omega} \frac{1}{2} [\alpha \cdot \mathbf{u}^{\circ 2} + \beta \cdot (\nabla \mathbf{u})^{\circ 2}] d\mathbf{r}}_{\text{Regularization term } (E_{\text{reg}})}.$$

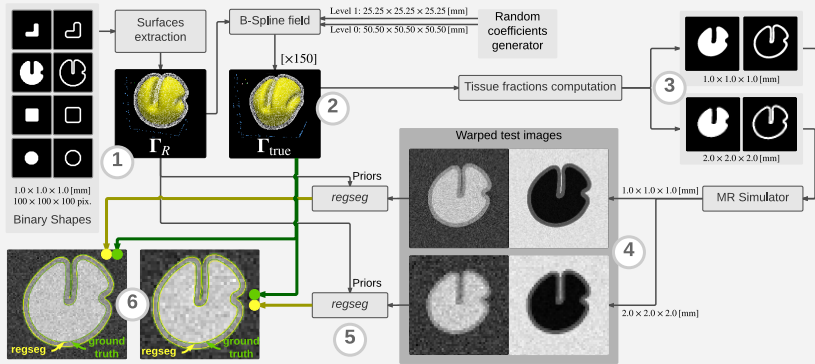
- Gradient-descent minimization:

$$\begin{aligned} \frac{\partial \mathbf{u}(\mathbf{r}, t)}{\partial t} &\propto - \frac{\partial E(\mathbf{u})}{\partial \mathbf{u}_k}, \\ \frac{\partial E(\mathbf{u})}{\partial \mathbf{u}_k} &= \frac{\partial E_{\text{data}}}{\partial \mathbf{u}_k} + \frac{\partial E_{\text{reg}}}{\partial \mathbf{u}_k} = \mathbf{g}_k + \frac{\partial E_{\text{reg}}}{\partial \mathbf{u}_k} \end{aligned}$$

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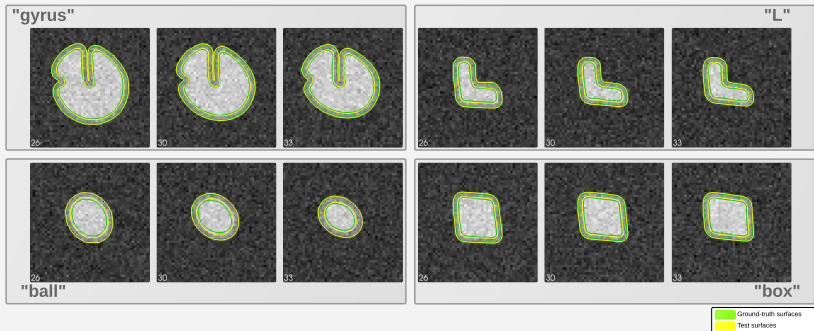
Validating regseg on phantoms (methods)

- **Random distortions:** 1200 experiments (4 model types \times 150 realizations of distortion \times 2 resolutions).
- **Bivariate target-image:** stack of T1w-like and T2w-like.
- **Segmentation model:** 2 surfaces, 3 regions (WM-like, GM-like crust, CSF-like background).



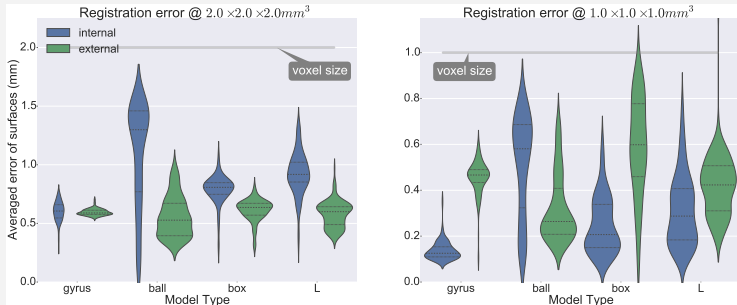
Validating regseg on phantoms (visual)

- **Visual assessment** (coronal views, $x = (26, 30, 33)$ of one deformation of each model):

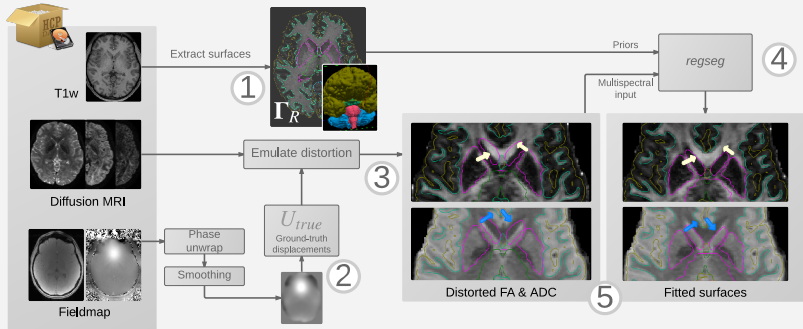


Validating regseg on phantoms (quantitative)

- Registration error measured with **Hausdorff distance** between ground-truth surfaces and those mapped with *regseg*.

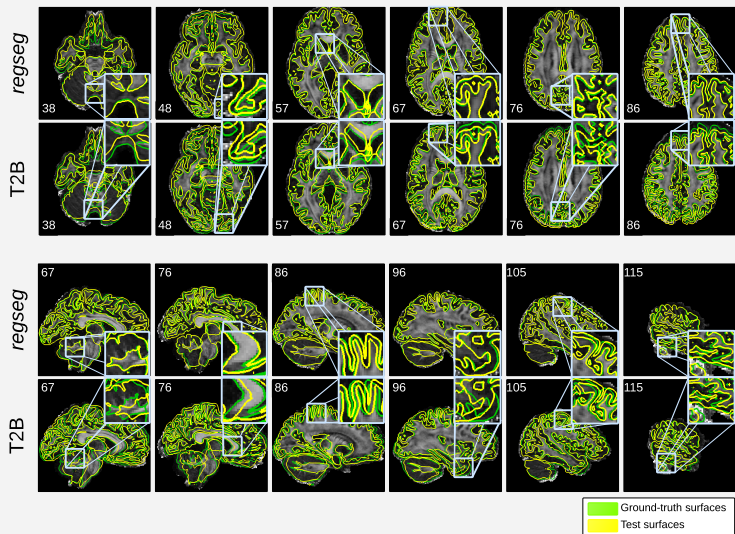


Using regseg on real datasets (methods)



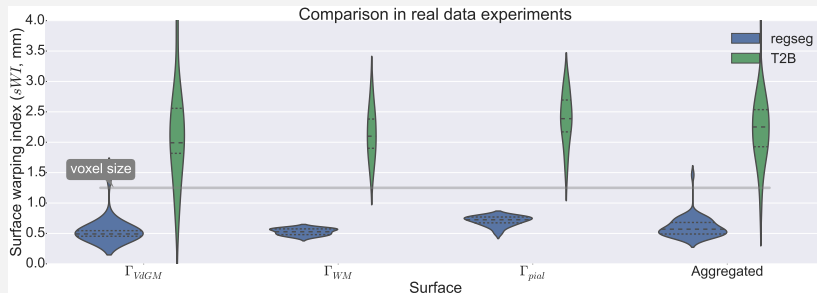
- An equivalent workflow was implemented to run a competing method, a T2-weighted to $b0$ registration method (*T2B correction*).
- T2B method configured using *ExploreDTI* (Leemans et al., 2009) settings.
- U_{true} is computed using the fieldmap.

Example report of regseg vs. T2B



Quantitative comparison of regseg vs. T2B

- ▶ 16 datasets from the HCP
- ▶ Since displacements happen only in y : evaluated the surface warping index (sWI).
- ▶ *regseg* performed significantly better than T2B ($p < 10^{-4}$).



Background and motivation

Context

Acquisition of diffusion MRI

Problems and challenges in
connectome extraction

Motivation and Objectives

Impact of susceptibility-derived
distortion and correction on simple
networks

Gold standards

Experiments and results

Diffantom: a digital whole-brain dMRI
dataset

Real Data

Microstructural model

Workflow

Generated datasets

Comparing SDCs at the scale of
whole-brain

The PySDCev evaluation framework

Geometrical accuracy

Impact on reconstruction,
tractography and networks

Regseg, a simultaneous registration
and segmentation method

Methods

Experiments on phantoms

Experiments on real datasets

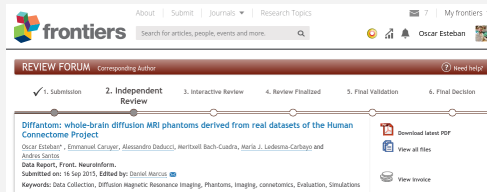
Conclusions and contributions

Publications

Contributions: whole-brain and ground-truth data

1. *Diffantom*: **a whole-brain dMRI phantom** derived from real datasets, designed for the assessment of processing tasks and full connectivity pipelines.

- We extended *Phantomas*, an existing software to generate dMRI phantoms with analytical fiber geometries, to produce whole-brain data.
- We defined an underlying microstructural model to simulate dMRI phantoms using the hindered and restricted diffusion model of *Phantomas*.
- We publicly release the first *Diffantom*, along with the *diffantomizer* that is the workflow to generate *diffantoms* from HCP datasets.
- Open-sourced.



Contributions: an evaluation framework

2. *PySDCev*: **a comprehensive evaluation framework** for the investigation of susceptibility-derived distortions and the comparison of retrospective correction methods.

- ▶ We demonstrated the impact of susceptibility distortion on brain networks.
- ▶ We assessed the accurate performance of three SDC methods recovering the distorted anatomy on dMRI images.
- ▶ We demonstrated the importance of working on native dMRI space.
- ▶ Partially open-sourced, awaiting publication.

Contributions: regseg applied in diffusion MRI

3. We propose *regseg*: **a nonlinear, surface-to-image registration method based on active contours without edges**. The method successfully maps a number of closed surfaces implemented explicitly with 3D meshes into a target image.

- Verified on phantoms.
- Applied on dMRI datasets.
- Sub-voxel accuracy.
- Open-sourced.

New Results

Surface-driven registration method for the structure-informed segmentation of diffusion MR images

Oscar Esteban, Dominique Zosso, Alessandro Daducci, Meritxell Bach-Cuadra, Maria J. Ledesma-Carbayo, Jean-Philippe Thiran, Andres Santos
doi: <http://dx.doi.org/10.1101/018945>

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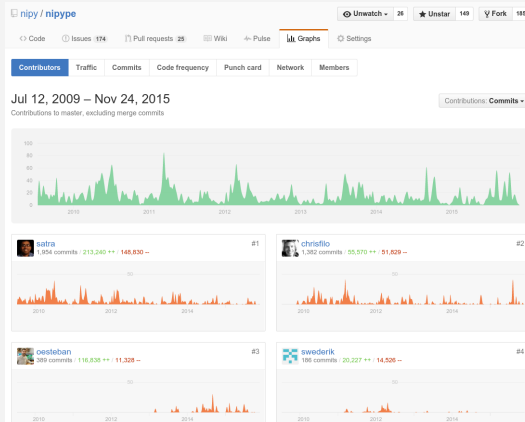
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Total	764	179

- Suitable in applications where we have **precise surfaces** of structures that need be fitted into **multivariate data** and the underlying deformation encodes some **important information** (development, evolution of pathology, etc.)



Contributions: pipelines and experimental instrumentation

4. Important contributions to third-party and open-source tools for dMRI data processing and pipelining of neuroimage processing tools.



Future lines

- ▶ **Implementing a new segmentation model working directly on the DWIs for *regseg*.** A recent method proposed by Jeurissen, Tournier, and Sijbers, 2015 uses non-negative matrix factorization of multi-shell dMRI data for tissue-type segmentation.
- ▶ **Integrating *regseg* in *PySDCev*.** Currently, *PySDCev* is designed to evaluate SDCs on the undistorted reference grid.
- ▶ **Generating a larger sample of *diffantoms*.** With the *Diffantom* presented in this dissertation, only one-subject experiments can be performed with *PySDCev*. This is an important limitation easily solvable with computing capacity, since each *Diffantom* takes around 12 days in an 8-core Intel® Xeon® CPU E31245 @ 3.30GHz, 32GB RAM.
- ▶ **Enlarging the number of network metrics tested by *PySDCev*.** Even though we tested the distortion impact on the network densities and the average of clustering coefficients, many more network measures (Duda, Cook, and Gee, 2014) should be included into *PySDCev*, for a better understanding of the confounding factors introduced with distortion.

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- Experiments on real datasets

- Conclusions and contributions

- Publications

Publications supporting this Ph.D. Thesis

- ▶ Esteban O., Caruyer E., Daducci A., Bach-Cuadra M., Ledesma-Carbayo M.-J., Santos A., *Diffantom: whole-brain diffusion MRI phantoms derived from real datasets of the Human Connectome Project*, Front. Neuroinf. (in revision), 2015. doi:10.1101/026898. (Ch. 4)
- ▶ Esteban O., Daducci A., Bach-Cuadra M., Ledesma-Carbayo M.-J., Santos A., *PySDCev: A framework to evaluate retrospective correction methods of susceptibility distortion in diffusion MRI*, Magn Res Med (in preparation), 2015. (Ch. 5)
- ▶ Esteban O., Zosso D., Daducci A., Bach-Cuadra M., Ledesma-Carbayo M.-J., Thiran J.-P., Santos A., *Surface-driven registration method for the structure-informed segmentation of diffusion MR images*, NeuroImage (in revision), 2015. doi:10.1101/018945. (Ch. 6)
- ▶ Esteban O., Wollny G., Gorthi S., Ledesma-Carbayo M.-J., Thiran J.-P., Santos A., Bach-Cuadra M., *MBIS: Multivariate Bayesian Image Segmentation Tool*, Comp Meth Prog Biomed 115(2):76–95. 2014. doi:10.1016/j.cmpb.2014.03.003. (Ch. 6)
- ▶ Esteban O., Daducci A., Caruyer E., O'Brien K., Ledesma-Carbayo M.-J., Bach-Cuadra M., Santos A., *Simulation-based evaluation of susceptibility distortion correction methods in diffusion MRI for connectivity analysis*, in 11th ISBI, Beijing, China. 2014. doi:10.1109/ISBI.2014.6867976. (Ch. 3)
- ▶ Martí-Fuster, Esteban O., Thielemans K., Setoain X., Santos A., Ros D., Pavia J., *Including anatomical and functional information in MC simulation of PET and SPECT brain studies. Brain-UISET: a voxel-based iterative method.*, IEEE Trans Med Imag 33(10):1931–1938. 2014. doi:10.1109/TMI.2014.2326041.
- ▶ Bach-Cuadra M., Gelin S., Roche A., Esteban O., Kober T., Marques J., Granziera C., Kreger G., *Classical Segmentation Methods on Novel MR Imaging: A Study of Brain Tissue Segmentation of MP2RAGE Vs MPRAGE*, in 21th ISMRM, p. 948, Salt Lake City, US. 2013.
- ▶ Martí-Fuster, Esteban O., Planes X., Aguiar P., Crespo C., Falcon C., Wollny G., Rubí S., Setoain X., Franji F., Ledesma-Carbayo M.-J., Santos A., Pavia J., Ros D., *FocusDET, A New Toolbox for SISCOM Analysis. Evaluation of the Registration Accuracy Using Monte Carlo Simulation*, Neuroinf. 11(1):77–89. 2013. doi:10.1007/s12021-012-9158-x.
- ▶ Kober T., Roche A., Esteban O., Gorthi S., Ribes D., Bach-Cuadra M., Meuli R., Kreger G., *Atlas-free Brain Tissue Segmentation Using a Single T1-weighted MRI Acquisition*, in 20th ISMRM, p. 753, Melbourne, Australia. 2012.

Thanks



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Image processing methods for human brain connectivity analysis from in-vivo diffusion MRI

Ph.D. Thesis

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November 25th, 2015